```
================================================================
Sequence Listing could not be accepted.
If you need help call the Patent Electronic Business Center at (866)
217-9197 (toll free).
Reviewer: Anne Corrigan
Timestamp: [year=2010; month=1; day=19; hr=10; min=55; sec=46; ms=248; ]
================================================================



****************************************************************
Reviewer Comments:
<210>   1
<211>   776
<212>   PRT
<213>   mammalian

The above <213> response is invalid, per 1.823 of the Sequence Rules.
The only valid responses are:  the Genus species of the organism,
"Artificial Sequence," or "Unknown".  "Artificial Sequence" and
"Unknown" require explanation in the <220>-<223> section; please
indicste the source of the genetic material.  For example, "mammalian"
would be an acceptable explanation for "Unknown".  Same error in
Sequence 2.


<210>   11
<211>   14
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   peptide


<400>   11



As an explanation of "<213> Artificial Sequence", the above <223>
response is insufficient.  The sequence is obviously a peptide sequence.
 Please indicate the source of the genetic material; same error in
Sequences 12-14.
****************************************************************
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            Validated By CRFValidator v 1.0.3

Application No:                              Version No:
                    10568396                                 3.0



                Input Set:


                Output Set:




            Started:    2009-12-30 18:59:37.288
           Finished:    2009-12-30 18:59:38.532
            Elapsed:    0 hr(s) 0 min(s) 1 sec(s) 244 ms
     Total Warnings:    14
       Total Errors:    0
No. of SeqIDs Defined:  14
   Actual SeqID Count:  14

Error code      Error Description

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W   402         Undefined organism found in <213>  in SEQ ID (2)

W   213         Artificial or Unknown found in <213>  in SEQ ID (3)

W   213         Artificial or Unknown found in <213>  in SEQ ID (4)

W   213         Artificial or Unknown found in <213>  in SEQ ID (5)

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W   213         Artificial or Unknown found in <213>  in SEQ ID (8)

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W   213         Artificial or Unknown found in <213>  in SEQ ID (11)

W   213         Artificial or Unknown found in <213>  in SEQ ID (12)

W   213         Artificial or Unknown found in <213>  in SEQ ID (13)

W   213         Artificial or Unknown found in <213>  in SEQ ID (14)
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SEQUENCE LISTING

<110>   THE TRUSTEES OF COLUMBIA UNIVERSITY IN THE CITY OF NEW YORK

<120>   ZAP PROTEIN AND RELATED COMPOSITIONS AND METHODS

<130>   67489-PCT/JPW/JW

<140>   10568396
<141>   2006-08-31

<150> PCT/US2004/026162
<151>   2004-08-12

<160>   14

<170>   PatentIn version 3.5

<210>   1
<211>   776
<212>   PRT
<213>   mammalian

<400>   1

Met Ala Asp Pro Gly Val Cys Cys Phe Ile Thr Lys Ile Leu Cys Ala
1   5   10   15

His Gly Gly Arg Met Thr Leu Glu Glu Leu Leu Gly Glu Ile Arg Leu
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Pro Glu Ala Gln Leu Tyr Glu Leu Leu Glu Thr Ala Gly Pro Asp Arg
        35   40   45

Phe Val Leu Leu Glu Thr Gly Gly Gln Ala Gly Ile Thr Arg Ser Val
    50   55   60

Val Ala Thr Thr Arg Ala Arg Val Cys Arg Arg Lys Tyr Cys Gln Arg
65   70   75   80

Pro Cys Asp Ser Leu His Leu Cys Lys Leu Asn Leu Leu Gly Arg Cys
            85   90   95

His Tyr Ala Gln Ser Gln Arg Asn Leu Cys Lys Tyr Ser His Asp Val
            100   105   110

Leu Ser Glu Gln Asn Phe Gln Ile Leu Lys Asn His Glu Leu Ser Gly
        115   120   125

Leu Asn Gln Glu Glu Leu Ala Cys Leu Leu Val Gln Ser Asp Pro Phe
    130   135   140

Phe Leu Pro Glu Ile Cys Lys Ser Tyr Lys Gly Glu Gly Arg Lys Gln
145   150   155   160

Thr Cys Gly Gln Pro Gln Pro Cys Glu Arg Leu His Ile Cys Glu His
                 165   170   175

Phe Thr Arg Gly Asn Cys Ser Tyr Leu Asn Cys Leu Arg Ser His Asn
                 180   185   190

Leu Met Asp Arg Lys Val Leu Thr Ile Met Arg Glu His Gly Leu Ser
        195   200   205

Pro Asp Val Val Gln Asn Ile Gln Asp Ile Cys Asn Asn Lys His Ala
    210   215   220

Arg Arg Asn Pro Pro Gly Thr Arg Ala Ala His Pro His Arg Arg Gly
225   230   235   240

Gly Ala His Arg Asp Arg Ser Lys Ser Arg Asp Arg Phe Leu His Asn
                 245   250   255

Ser Leu Glu Phe Leu Ser Pro Val Val Ser Pro Leu Gly Ser Gly Pro
                 260   265   270

Pro Ser Pro Asp Val Thr Ser Cys Lys Asp Ser Leu Glu Asp Val Ser
        275   280   285

Val Asp Val Thr Gln Lys Phe Lys Tyr Leu Gly Thr His Asp Arg Ala
    290   295   300

Gln Leu Ser Pro Val Ser Ser Lys Ala Ala Gly Val Gln Gly Pro Ser
305   310   315   320

Gln Met Arg Ala Ser Gln Glu Phe Ser Glu Asp Gly Asn Leu Asp Asp
                 325   330   335

Ile Phe Ser Arg Asn Arg Ser Asp Ser Ser Ser Ser Arg Ala Ser Ala
                 340   345   350

Ala Lys Val Ala Gln Arg Asn Glu Ala Val Ala Met Lys Met Gly Met

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                355                      360                      365

Glu Val Lys Gly Lys Lys Glu Ala Pro Asp Ile Asp Arg Val Pro Phe
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385                   390                   395                   400

Gly Ile Pro Gly Lys Lys Phe Thr Ala Asn Asp Leu Glu Asn Leu Leu
              405                   410                   415

Leu Leu Asn Asp Thr Trp Lys Asn Val Ala Lys Pro Gln Asp Leu Gln
              420                   425                   430

Thr Thr Gly Arg Ile Thr Asp Ser Gly Gln Asp Lys Ala Phe Leu Gln
          435                   440                   445

Asn Lys Tyr Gly Gly Asn Pro Val Trp Ala Ser Ala Ser Thr His Asn
   450                   455                   460

Ala Pro Asn Gly Ser Ser Gln Ile Met Asp Glu Thr Pro Asn Val Ser
465                   470                   475                   480

Lys Ser Ser Thr Ser Gly Phe Ala Ile Lys Pro Ala Ile Ala Gly Gly
              485                   490                   495

Lys Glu Ala Val Tyr Ser Gly Val Gln Ser Pro Arg Ser Gln Val Leu
          500                   505                   510

Ala Val Pro Gly Glu Ala Thr Thr Pro Val Gln Ser Asn Arg Leu Pro
          515                   520                   525

Gln Ser Pro Leu Ser Ser Ser Ser His Arg Ala Ala Ala Ser Gly Ser
   530                   535                   540

Pro Gly Lys Asn Ser Thr His Thr Ser Val Ser Pro Ala Ile Glu Ser
545                   550                   555                   560

Ser Arg Met Thr Ser Asp Pro Asp Glu Tyr Leu Leu Arg Tyr Ile Leu
              565                   570                   575

Asn Pro Leu Phe Arg Met Asp Asn His Gly Pro Lys Glu Ile Cys Gln
              580                   585                   590
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Asp His Leu Tyr Lys Gly Cys Gln Gln Ser His Cys Asp Arg Ser His
        595   600   605

Phe His Leu Pro Tyr Arg Trp Gln Met Phe Val Tyr Thr Thr Trp Arg
    610   615   620

Asp Phe Gln Asp Met Glu Ser Ile Glu Gln Ala Tyr Cys Asp Pro His
625   630   635   640

Val Glu Leu Ile Leu Ile Glu Asn His Gln Ile Asn Phe Gln Lys Met
                645   650   655

Thr Cys Asp Ser Tyr Pro Ile Arg Arg Leu Ser Thr Pro Ser Tyr Glu
        660   665   670

Glu Lys Pro Leu Ser Ala Val Phe Ala Thr Lys Trp Ile Trp Tyr Trp
        675   680   685

Lys Asn Glu Phe Asn Glu Tyr Ile Gln Tyr Gly Asn Glu Ser Pro Gly
    690   695   700

His Thr Ser Ser Asp Ile Asn Ser Ala Tyr Leu Glu Ser Phe Phe Gln
705   710   715   720

Ser Cys Pro Arg Gly Val Leu Pro Phe Gln Ala Gly Ser Gln Lys Tyr
                725   730   735

Glu Leu Ser Phe Gln Gly Met Ile Gln Thr Asn Ile Ala Ser Lys Thr
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Gln Arg His Val Val Arg Arg Pro Val Phe Val Ser Ser Asn Asp Val
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<213>   mammalian

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actcggtctg tagtggctac tactcgagcc cgcgtctgcc gtcggaagta ctgccagaga        240

ccctgcgaca gcctgcacct ctgcaagctt aatctgctcg gccggtgcca ctatgcacag        300

tctcagcgga acctctgcaa atattctcac gatgttctct cggaacagaa cttccagatc        360

ctgaagaatc atgagctctc tgggcttaac caagaggagc tagcttgcct cctggtccaa        420

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acctgtgggc agccacagcc atgcgagaga ctccacatct gtgagcactt cacccggggc        540

aactgcagtt acctcaactg tctcaggtct cacaacctga tggacagaaa ggtgttgacc        600

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ctctcacctg ttgtctcacc tctgggatct ggtccgccta gcccagatgt caccagctgt        840

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catgaccgtg cgcagctctc cccagtctca tctaaggctg ctggtgttca aggacccagt        960

caaatgagag caagccaaga gttttcagag gatgggaatc tagatgacat attttctagg       1020

aatcgttctg attcatcatc aagtcgagcc tccgctgcca aggtggcaca aagaaatgaa       1080

gctgtggcca tgaaaatggg catggaggtc aagggcaaga aggaggctcc agacatcgat       1140

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ggaattccag gcaaaaagtt cacagccaat gatctggaaa atttgctatt acttaacgac       1260

acttggaaga atgtggctaa gccccaggat ctgcagacca caggcagaat cactgacagt       1320

ggccaagaca aggcattcct gcagaataaa tatggaggaa acccagtgtg ggcaagtgca       1380

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cctgtacaga gcaacaggct gcctcagtcg cctctgtctt cctcaagcca cagagctgca       1620

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tcaaggatga catcagaccc cgatgagtat ctcctacgct acatcctaaa tccttttattt       1740
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aggatggata atcatggccc gaaggaaatc tgtcaggacc atctgtacaa gggctgtcaa   1800

cagagccact gcgacaggag tcacttccat ctgccctacc ggtggcagat gttcgtatat   1860

accacttgga gggacttcca ggacatggag tctatcgaac aggcctattg tgatccccac   1920

gttgaactca ttttgataga aaaccatcag atcaatttcc agaaaatgac ctgtgactcc   1980

taccccatcc gacgcctctc cactccctca tatgaggaaa agccacttag tgctgtcttc   2040

gccaccaagt ggatttggta ttggaagaat gaatttaatg aatatatcca gtatgggaat   2100

gagagcccag gccacaccag ctctgacatc aactctgcgt acctggagtc tttcttccag   2160

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caagggatga ttcagacaaa tatagcttcc aagactcaaa ggcatgttgt cagaaggcca   2280

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<213> Artificial Sequence

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cgccaagttg accagtgc   78

<210> 4
<211> 26
<212> DNA
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<220>
<223> PCR Primer

<400> 4
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<210> 5
<211> 38
<212> DNA
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<220>
<223> Oligonucleotide

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<210> 6
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Oligonucleotide

<400> 6
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<210> 7
<211> 25
<212> DNA
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<220>
<223> PCR Primer

<400> 7
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<210> 8
<211> 34
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<223> PCR Primer

<400> 8
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<210> 9
<211> 19
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<400> 9
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<210> 10
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<220>
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<400> 10

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<210> 11
<211> 14
<212> PRT
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<220>
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<400> 11

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<210> 12
<211> 23
<212> PRT
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<220>
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<400> 12

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<210> 13
<211> 23
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<400> 13

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Gln Pro Cys Glu Arg Leu His
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<210> 14
<211> 18

<212> PRT
<213> Artificial Sequence

<220>
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<400> 14

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Ser His